AMENDMENTS TO THE CLAIMS:

1-16 (canceled)

17. (currently amended) A method of determining the suitability of a patient for radiation therapy, the method comprising:

predicting whether a subject will be susceptible to undesirable toxicity resulting from treatment with radiation therapy, said method comprising:

(a) obtaining ~~an~~ transcriptional expression profile for the response to radiation for a sample from said subject for at least 10 sequences selected from ~~the 50 top ranked genes set forth in Table 3 from said subject~~ M25753, HUMCYCB; AI436567, ATP5D; X54942, CKS2; AB011126, FBP17; U14971, RPS9; AL022318, MDS019; L08096, TNFSF7; AL080113; AI126004, SAS10; Z23090, HSPB1; D21090, RAD23B; U35451, CBX1; AA890010; M65028, HNRPAB; D26600, PSMB4; AF072810, BAZ1B; U49869; D16581, NUDT1; AA121509, LOC51690; X81625, ETF1; Z48501, PABPC1; AA121509, LOC51690; U12022, CALM1; U52682, IRF4; J03592, SLC25A6; J03161, SRF; Z11692, EEF2; X83218, ATP5O; X51688, CCNA2; U11861, G10; D44466, PSMD1; AB019392, M9; AI991040, DRAP1; X70944, SFPQ; M25753; X15414, AKR1B1; U12779, MAPKAPK2; Z49254, MRPL23; J02683, SLC25A5; S87759, PPM1A; D32050, AARS; X06617, RPS11; AF023676, TM7SF2; AB002368, KIAA0370; AB029038, KIAA1115; D45248, PSME2; D13641, KIAA0016; M58378; Y18418, RUVBL1; and L20298, CBFB; and

(b) comparing said obtained expression profile to a reference expression profile from a cell known to have a susceptible phenotype for radiation toxicity to determine the probability that said patient is susceptible to undesirable radiation toxicity;

wherein a patient that is predicted to have a high probability of undesirable radiation toxicity is less suitable for radiation therapy.

18-19. (canceled)

20. (withdrawn, currently amended) The method according to Claim 17, wherein said expression profile ~~comprises at least 25 sequences selected from the 50 top ranked genes set forth in Table 3~~ includes expression data from M25753, HUMCYCB; AI436567, ATP5D; X54942, CKS2; AB011126, FBP17; U14971, RPS9; AL022318, MDS019; L08096, TNFSF7; AL080113; AI126004, SAS10; Z23090, HSPB1; D21090, RAD23B; U35451, CBX1; AA890010; M65028, HNRPAB; D26600, PSMB4; AF072810, BAZ1B; U49869; D16581, NUDT1; AA121509, LOC51690; X81625, ETF1; Z48501, PABPC1; AA121509, LOC51690; U12022, CALM1; U52682, IRF4; J03592, SLC25A6; J03161, SRF;

Z11692, EEF2; X83218, ATP5O; X51688, CCNA2; U11861, G10; D44466, PSMD1; AB019392, M9; AI991040, DRAP1; X70944, SFPQ; M25753; X15414, AKR1B1; U12779, MAPKAPK2; Z49254, MRPL23; J02683, SLC25A5; S87759, PPM1A; D32050, AARS; X06617, RPS11; AF023676, TM7SF2; AB002368, KIAA0370; AB029038, KIAA1115; D45248, PSME2; D13641, KIAA0016; M58378; Y18418, RUVBL1; and L20298, CBFB.

21. (original) The method according to Claim 17, wherein said undesirable toxicity is at least a grade 2 toxicity.

22. (currently amended) A method of determining the suitability of a patient for treatment with an anti-proliferative chemotherapeutic agent that induces double-stranded breaks in DNA, the method comprising:

predicting whether a subject will be susceptible to undesirable toxicity resulting from treatment with said chemotherapeutic agent, said method comprising:

(a) obtaining ~~an~~ transcriptional expression profile for the response to said chemotherapeutic agent for a sample from said subject for at least 10 sequences selected from ~~the 50 top ranked genes set forth in Table 3 from said subject~~ M25753, HUMCYCB; AI436567, ATP5D; X54942, CKS2; AB011126, FBP17; U14971, RPS9; AL022318, MDS019; L08096, TNFSF7; AL080113; AI126004, SAS10; Z23090, HSPB1; D21090, RAD23B; U35451, CBX1; AA890010; M65028, HNRPAB; D26600, PSMB4; AF072810, BAZ1B; U49869; D16581, NUDT1; AA121509, LOC51690; X81625, ETF1; Z48501, PABPC1; AA121509, LOC51690; U12022, CALM1; U52682, IRF4; J03592, SLC25A6; J03161, SRF; Z11692, EEF2; X83218, ATP5O; X51688, CCNA2; U11861, G10; D44466, PSMD1; AB019392, M9; AI991040, DRAP1; X70944, SFPQ; M25753; X15414, AKR1B1; U12779, MAPKAPK2; Z49254, MRPL23; J02683, SLC25A5; S87759, PPM1A; D32050, AARS; X06617, RPS11; AF023676, TM7SF2; AB002368, KIAA0370; AB029038, KIAA1115; D45248, PSME2; D13641, KIAA0016; M58378; Y18418, RUVBL1; and L20298, CBFB; and

(b) comparing said obtained expression profile to a reference expression profile from a cell known to have a susceptible phenotype for toxicity from the chemotherapeutic agent to determine the probability that said patient is susceptible to undesirable toxicity;

wherein a patient that is predicted to have a high probability of undesirable toxicity is less suitable for said treatment with an anti-proliferative chemotherapeutic agent.

23. (currently amended) A method of optimizing anti-proliferative therapy for a patient, the method comprising:

(a) obtaining ~~an~~ transcriptional expression profile for the response to said anti-proliferative therapy for a sample from said subject for at least 10 sequences selected from ~~the 50 top ranked genes set forth in Table 3 from said subject~~ M25753, HUMCYCB; AI436567, ATP5D; X54942, CKS2; AB011126, FBP17; U14971, RPS9; AL022318, MDS019; L08096, TNFSF7; AL080113; AI126004, SAS10; Z23090, HSPB1; D21090, RAD23B; U35451, CBX1; AA890010; M65028, HNRPAB; D26600, PSMB4; AF072810, BAZ1B; U49869; D16581, NUDT1; AA121509, LOC51690; X81625, ETF1; Z48501, PABPC1; AA121509, LOC51690; U12022, CALM1; U52682, IRF4; J03592, SLC25A6; J03161, SRF; Z11692, EEF2; X83218, ATP5O; X51688, CCNA2; U11861, G10; D44466, PSMD1; AB019392, M9; AI991040, DRAP1; X70944, SFPQ; M25753; X15414, AKR1B1; U12779, MAPKAPK2; Z49254, MRPL23; J02683, SLC25A5; S87759, PPM1A; D32050, AARS; X06617, RPS11; AF023676, TM7SF2; AB002368, KIAA0370; AB029038, KIAA1115; D45248, PSME2; D13641, KIAA0016; M58378; Y18418, RUVBL1; and L20298, CBFB; and

(b) comparing said obtained expression profile to a reference expression profile from a cell known to have a susceptible phenotype for toxicity from the anti-proliferative therapy to determine the probability that said patient is susceptible to undesirable toxicity;

wherein a dose of said anti-proliferative therapy is selected to minimize to undesirable toxicity, while providing for effective anti-proliferative activity.

24-25. (canceledl)

26. (currently amended) A method of obtaining an expression profile for the transcriptional response to radiation, the method comprising:

exposing a cell sample from an individual to radiation;

extracting mRNA from said cell;

quantitating the level of mRNA corresponding at least 10 sequences selected from the 50 top ranked genes set forth in Table 3;

comparing said level of mRNA to the level of said mRNA present in a cell sample from said individual not exposed to radiation, wherein said comparing step comprises a nearest shrunken centroid analysis step.

27. (original) The method according to Claim 26, wherein said exposing to radiation comprises exposes said cell to a dose of ionizing radiation of from about 2 to about 10 Gy.

28. (original) The method according to Claim 27, wherein said mRNA is extracted after at least about 2 and not more than about 24 hours following said exposure.

29. (original) The method according to Claim 27, further comprising exposing a cell sample from said individual to ultraviolet radiation at a dose of at least about 5 J/m^2 and not more than about 50 J/m^2.

30. (original) The method according to Claim 29, wherein said mRNA is extracted after at least about 4 and not more than about 72 hours following said exposure.

31. (canceled)

32. (original) A method of obtaining an expression profile for the transcriptional response in a phenotype of interest, the method comprising:

exposing a cell sample from an individual to said anti-proliferative therapy;

extracting mRNA from said cell;

quantitating the level of mRNA corresponding to a sequence of interest;

comparing by nearest shrunken centroid analysis said level of mRNA to the level of said mRNA present in a cell sample from said individual not exposed to said anti-proliferative therapy.

33. (original) The method according to Claim 32, wherein said phenotype of interest comprises anti-proliferative therapy.

34-46. (canceled)

47. The method of Claim 17, wherein the comparing step is performed with shrunken centroid analysis.

48. (new) The method of Claim 22, wherein said expression profile includes expression data from M25753, HUMCYCB; AI436567, ATP5D; X54942, CKS2; AB011126, FBP17; U14971, RPS9; AL022318, MDS019; L08096, TNFSF7; AL080113; AI126004, SAS10; Z23090, HSPB1; D21090, RAD23B; U35451, CBX1; AA890010; M65028, HNRPAB; D26600, PSMB4; AF072810, BAZ1B; U49869;

D16581, NUDT1; AA121509, LOC51690; X81625, ETF1; Z48501, PABPC1; AA121509, LOC51690; U12022, CALM1; U52682, IRF4; J03592, SLC25A6; J03161, SRF; Z11692, EEF2; X83218, ATP5O; X51688, CCNA2; U11861, G10; D44466, PSMD1; AB019392, M9; AI991040, DRAP1; X70944, SFPQ; M25753; X15414, AKR1B1; U12779, MAPKAPK2; Z49254, MRPL23; J02683, SLC25A5; S87759, PPM1A; D32050, AARS; X06617, RPS11; AF023676, TM7SF2; AB002368, KIAA0370; AB029038, KIAA1115; D45248, PSME2; D13641, KIAA0016; M58378; Y18418, RUVBL1; and L20298, CBFB.

49 (new) The method of Claim 48, wherein the comparing step is performed with shrunken centroid analysis.

50 (new) The method of Claim 23, wherein said expression profile includes expression data from M25753, HUMCYCB; AI436567, ATP5D; X54942, CKS2; AB011126, FBP17; U14971, RPS9; AL022318, MDS019; L08096, TNFSF7; AL080113; AI126004, SAS10; Z23090, HSPB1; D21090, RAD23B; U35451, CBX1; AA890010; M65028, HNRPAB; D26600, PSMB4; AF072810, BAZ1B; U49869; D16581, NUDT1; AA121509, LOC51690; X81625, ETF1; Z48501, PABPC1; AA121509, LOC51690; U12022, CALM1; U52682, IRF4; J03592, SLC25A6; J03161, SRF; Z11692, EEF2; X83218, ATP5O; X51688, CCNA2; U11861, G10; D44466, PSMD1; AB019392, M9; AI991040, DRAP1; X70944, SFPQ; M25753; X15414, AKR1B1; U12779, MAPKAPK2; Z49254, MRPL23; J02683, SLC25A5; S87759, PPM1A; D32050, AARS; X06617, RPS11; AF023676, TM7SF2; AB002368, KIAA0370; AB029038, KIAA1115; D45248, PSME2; D13641, KIAA0016; M58378; Y18418, RUVBL1; and L20298, CBFB.

51 (new) The method of Claim 50, wherein the comparing step is performed with shrunken centroid analysis.